

Exhibit A

Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882

1.(previously amended) An isolated nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1.

2.(previously amended) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:2.

3.(original) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.

4.(original) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.

5.(original) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.

6. (original) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.

7.(previously added) An expression vector comprising a nucleic acid sequence of Claim 2.

8.(previously added) A cell comprising the expression vector of Claim 7.

Exhibit B

Clean version of title in
U.S. Patent Application Ser. No. 09/714,882

Human *Notch* Ligand Proteins and Polynucleotides Encoding the Same

Exhibit C

Marked-up version of title in
U.S. Patent Application Ser. No. 09/714,882

[Novel] Human *Notch* Ligand Proteins and Polynucleotides Encoding the Same

Exhibit D
BLAST result of SEQ ID NO:1 versus human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
33,840 sequences; 200,810,911,373 total letters

Query= LEX91seqid1
(2070 letters)

Sequences producing significant alignments:	Score bits)	E Value
---	----------------	------------

AL109657.8.1.100272	349	4e-93
AL117333.26.1.156813	339	4e-90

>AL109657.8.1.100272
Length = 100272

Score = 349 bits (176), Expect = 4e-93
Identities = 176/176 (100%)
Strand = Plus / Minus

Query: 1644 aggcaatgcatttgctagagtaaaaattggagattaccattactatggctatgggactaa
1703

|||||
Sbjct: 68087 aggcaatgcatttgctagagtaaaaattggagattaccattactatggctatgggactaa
68028

Query: 1704 gaaagactatcaaacagcagccacacactacagcattgcagccaacaaataccacaacgc
1763

|||||
Sbjct: 68027 gaaagactatcaaacagcagccacacactacagcattgcagccaacaaataccacaacgc
67968

Query: 1764 gcaagccatgttcaatctggcttatatgtatgaacacggcttaggcattcacaagg 1819

|||||
Sbjct: 67967 gcaagccatgttcaatctggcttatatgtatgaacacggcttaggcattcacaagg 67912

Score = 333 bits (168), Expect = 2e-88
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 1403 agctttataaaaggtgtctgtgaactaggccactgggctgagaaattcctgacagcttact 1462

|||||
Sbjct: 74167 agctttataaaaggtgtctgtgaactaggccactgggctgagaaattcctgacagcttact 74108

Query: 1463 ttgcctataaggatggtgatatagattcttctcttgttcagtatgcactgcttgcagaaa 1522

|||||
Sbjct: 74107 ttgcctataaggatggtgatatagattcttctcttgttcagtatgcactgcttgcagaaa 74048

Query: 1523 tgggggtatgaagtagctcaaagcaattcagcattcattttggaatcta 1570

|||||
Sbjct: 74047 tgggggtatgaagtagctcaaagcaattcagcattcattttggaatcta 74000

Score = 311 bits (157), Expect = 9e-82
Identities = 157/157 (100%)
Strand = Plus / Minus

Query: 746 ttgctgacacatttgaaaaaagtgaaggtgttccagtggaaaaagtgagactaacggaaa 805

|||||
Sbjct: 95093 ttgctgacacatttgaaaaaagtgaaggtgttccagtggaaaaagtgagactaacggaaa 95034

Query: 806 gacctgaaaatctgagttctaacagtgagattttggattgggacatataccaataactata 865

|||||
Sbjct: 95033 gacctgaaaatctgagttctaacagtgagattttggattgggacatataccaataactata 94974

Query: 866 aatttttggcagaaagaggagatgttcagatacaagt 902

|||||
Sbjct: 94973 aatttttggcagaaagaggagatgttcagatacaagt 94937

↑

Score = 288 bits (145), Expect = 1e-74
Identities = 148/149 (99%)
Strand = Plus / Minus

Query: 1256 ctggctctggaatatggaaggattataaacttgccttcaaataatttttacctggcatctc 1315

|||||
Sbjct: 75501 ctggctctggaatatggaaggattataaacttgccttcaaataatttttacctggcatctc 75442

Query: 1316 agagtgggcagcccctcgccatttattatctggccaagatgtatgcaacaggaacaggag 1375

Sbjct: 75441 ||||| agagtgggcagccccttgccatttattatctggccaagatgtatgcaacaggaacaggag
75382

Query: 1376 tagtaagatcatgcagaactgctgtggag 1404

Sbjct: 75381 ||||| tagtaagatcatgcagaactgctgtggag 75353

Score = 260 bits (131), Expect = 3e-66
Identities = 131/131 (100%)
Strand = Plus / Minus

Query: 1817 aggacattcacttggccagaagattgtacgacatggctgctcaaacgagtccagatgccc
1876

Sbjct: 58972 ||||| aggacattcacttggccagaagattgtacgacatggctgctcaaacgagtccagatgccc
58913

Query: 1877 acatacctgtgctctttgccgtcatgaaactggaaactacgcatttgctccgggatatcc
1936

Sbjct: 58912 ||||| acatacctgtgctctttgccgtcatgaaactggaaactacgcatttgctccgggatatcc
58853

Query: 1937 tgttttttaat 1947

Sbjct: 58852 ||||| tgttttttaat 58842

Score = 244 bits (123), Expect = 2e-61
Identities = 123/123 (100%)
Strand = Plus / Minus

Query: 1948 cagttcacacgagatggaactggctgaaactggacaacaccattggaccacactgggac
2007

Sbjct: 58258 ||||| cagttcacacgagatggaactggctgaaactggacaacaccattggaccacactgggac
58199

Query: 2008 ttatttgtgattggcctcattgttcctgggctgattttgttgcttagaaatcaccatggg
2067

Sbjct: 58198 ||||| ttatttgtgattggcctcattgttcctgggctgattttgttgcttagaaatcaccatggg
58139

Query: 2068 tag 2070
|||

Sbjct: 58138 tag 58136

Score = 173 bits (87), Expect = 5e-40
Identities = 88/89 (98%)
Strand = Plus / Minus

Query: 1167 gaattatgccraagcacttaaatactttcagaaagctgcggaaaaaggggtggccccgacgc
1226

|||||
Sbjct: 78242 gaattatgccgaagcacttaaatactttcagaaagctgcggaaaaaggggtggccccgacgc
78183

Query: 1227 acagttccagttaggcttcatgtactact 1255

|||||
Sbjct: 78182 acagttccagttaggcttcatgtactact 78154

Score = 165 bits (83), Expect = 1e-37
Identities = 87/88 (98%), Gaps = 1/88 (1%)
Strand = Plus / Minus

Query: 659 tttt-ggggtacagatatttgtcgggaatcaatgttctacagaattgtgaagttgcccta 717

|||||
Sbjct: 96507 ttttaggggtacagatatttgtcgggaatcaatgttctacagaattgtgaagttgcccta
96448

Query: 718 agttattacaagaaagtggcagattata 745

|||||
Sbjct: 96447 agttattacaagaaagtggcagattata 96420

Score = 161 bits (81), Expect = 2e-36
Identities = 81/81 (100%)
Strand = Plus / Minus

Query: 1025 agatgtatntagaggggaatgctgccgtgccgcaaaataacgctactgccttcaagtact
1084

|||||
Sbjct: 84768 agatgtatntagaggggaatgctgccgtgccgcaaaataacgctactgccttcaagtact
84709

Query: 1085 tttccatggcagccagtaagg 1105

|||||
Sbjct: 84708 tttccatggcagccagtaagg 84688

Score = 151 bits (76), Expect = 2e-33
Identities = 76/76 (100%)
Strand = Plus / Minus

Query: 1571 aaaaggctaacattcttgaaaaagagaagatgtatccaatggcgcttctcctatggaatc
1630
Sbjct: 73892 aaaaggctaacattcttgaaaaagagaagatgtatccaatggcgcttctcctatggaatc
73833

Query: 1631 gagctgccattcaagg 1646
Sbjct: 73832 gagctgccattcaagg 73817

Score = 137 bits (69), Expect = 3e-29
Identities = 69/69 (100%)
Strand = Plus / Minus

Query: 958 aaagcattacactacttcttaaaggcagcaaaggccgggagtgcaaatgccatggcattt
1017
Sbjct: 86239 aaagcattacactacttcttaaaggcagcaaaggccgggagtgcaaatgccatggcattt
86180

Query: 1018 ataggaaag 1026
Sbjct: 86179 ataggaaag 86171

Score = 129 bits (65), Expect = 7e-27
Identities = 65/65 (100%)
Strand = Plus / Minus

Query: 1103 agggcaatgcaatcggccttcatgggcttgggtcttctttactttcatggaaaaggagttc
1162
Sbjct: 78856 agggcaatgcaatcggccttcatgggcttgggtcttctttactttcatggaaaaggagttc
78797

Query: 1163 ccctg 1167
Sbjct: 78796 ccctg 78792

Score = 125 bits (63), Expect = 1e-25
Identities = 63/63 (100%)
Strand = Plus / Minus

Query: 602 aggcactgatataattacacctttggaagtgctggaggaaacatgatgtcccagatgattt 661
|||||
Sbjct: 96654 aggcactgatataattacacctttggaagtgctggaggaaacatgatgtcccagatgattt
96595

Query: 662 tgg 664
|||
Sbjct: 96594 tgg 96592

Score = 113 bits (57), Expect = 4e-22
Identities = 57/57 (100%)
Strand = Plus / Minus

Query: 901 gtctctcttggacaattacatctaattggcaggaaaggtctagatcaggattactac 957
|||||
Sbjct: 94054 gtctctcttggacaattacatctaattggcaggaaaggtctagatcaggattactac 93998

Score = 109 bits (55), Expect = 7e-21
Identities = 55/55 (100%)
Strand = Plus / Minus

Query: 550 gcattaggatTTTTgtcttcttatggaataggaatggaatatgatcaagctaagg 604
|||||
Sbjct: 97163 gcattaggatTTTTgtcttcttatggaataggaatggaatatgatcaagctaagg 97109

>AL117333.26.1.156813
Length = 156813

Score = 339 bits (171), Expect = 4e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

Query: 113 aggtatcagtgaacgaaatcaacaatatTTTatcacacatattggaacaaagaacatcta 172
|||||
Sbjct: 28470 aggtatcagtgaacgaaatcaacaatatTTTatcacacatattggaacaaagaacatcta
28411

Query: 173 gtaatgtaatcaataaaagagaaaatctcctggagaaaaagaagaatcaacgtaaaataa 232
|||||
Sbjct: 28410 gtaatgtaatcaataaaagagaaaatctcctggagaaaaagaagaatcaacgtaaaataa
28351

Query: 233 gaataaaaggaattcaaaataaagatatcttgaagagaaataagaatcatt 283

|||||
Sbjct: 28350 gaataaaaggaattcaaaataaagatatcttgaagagaaataagaatcatt 28300

Score = 325 bits (164), Expect = 6e-86
Identities = 164/164 (100%)
Strand = Plus / Minus

Query: 387 agcctacctactttttgccaaagcagctgacatgggaaacttgaaagctatggagaaaat 446
|||||
Sbjct: 10641 agcctacctactttttgccaaagcagctgacatgggaaacttgaaagctatggagaaaat
10582

Query: 447 ggctgacgcttttgctatttggaattttggcgtgcaaaatataacagcagctatccaatt 506
|||||
Sbjct: 10581 ggctgacgcttttgctatttggaattttggcgtgcaaaatataacagcagctatccaatt
10522

Query: 507 atatgagtccttggctaaagaaggatcatgtaaagcccaaaacg 550
|||||
Sbjct: 10521 atatgagtccttggctaaagaaggatcatgtaaagcccaaaacg 10478

Score = 204 bits (103), Expect = 2e-49
Identities = 103/103 (100%)
Strand = Plus / Minus

Query: 284 tacaaaagcaagcagagaaaaattttacagatgaaggagaccagctatttaagatgggca 343
|||||
Sbjct: 15820 tacaaaagcaagcagagaaaaattttacagatgaaggagaccagctatttaagatgggca
15761

Query: 344 tcaaggttctccagcagtcctaaaagccaaaaacaaaaagaaga 386
|||||
Sbjct: 15760 tcaaggttctccagcagtcctaaaagccaaaaacaaaaagaaga 15718

Score = 117 bits (59), Expect = 3e-23
Identities = 59/59 (100%)
Strand = Plus / Minus

Query: 59 ctatcaaagcagaggaacataataaaagacaaaaggaaagaatgtcaccacacaggta 117
|||||
Sbjct: 52828 ctatcaaagcagaggaacataataaaagacaaaaggaaagaatgtcaccacacaggta
52770

Score = 115 bits (58), Expect = 1e-22
Identities = 58/58 (100%)
Strand = Plus / Minus

Query: 1 atgaagcccttgtctctgttaatagagatattgataattcttgggggcacaattaaaa 58
|||||
Sbjct: 87231 atgaagcccttgtctctgttaatagagatattgataattcttgggggcacaattaaaa 87174